

Genetic dissection of spike productivity traits in spring barley

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Motivation and Aim: Barley (*Hordeum vulgare* L.) is one of the most commonly cultivated cereals worldwide. The total area occupied by this crop in Russia amounts to 8.8 million Ha. The main goal in barley breeding is to combine high yield with better grain quality. In Russia, the main areas are occupied by two-row barley. Six-row barley can be a carrier of many useful traits for the breeding process. The genes introgression that controls these traits to two-row varieties is a perspective task. When investigating the productivity traits related to the assessment of grain productivity, it is necessary to understand how much the loci that determine the spike row will affect this trait. The study of samples containing both two-row and six-row forms will allow us to identify new donors for breeding programs. An important task is to obtain the maximum possible yield with high grain quality.

Like other cultivated plants, barley requires constant improvement of varieties and adaptation to changing conditions. When breeding using traditional methods, the process of creating a variety includes many field tests and usually takes 12–15 years. Currently, selection methodology has been significantly enriched by the inclusion of genetic markers in the work. The most modern method is genome-wide association studies (GWAS), which is based on identifying SNPs associated with the desired trait. Over the past two decades, donor genetic diversity for various traits has been significantly expanded using GWAS.

The aim of this study is to identify loci associated with traits of barley grain productivity and to evaluate the influence of genes that control the number of rows in a spike on the studied phenotypes. The study examined traits that may affect productivity, such as “spike length”, “number of grains per main spike”, “weight of 1000 grains”, “grain weight of the main spike”. These characteristics are economically important because they are the main determinants of barley yield.

Methods and Algorithms: For candidate marker identification, the following analyses were carried out: phenotyping (structural), genotyping and association test. The genotyping was carried out using new chip Barley 50 K Illumina Infinium iSELECT. Using GWAS, significant SNPs associated with an agronomic trait were revealed over a three-year period. Then, we conducted association tests followed by meta-analysis of three years results. Based on the data obtained, a sample was created that included 129 only two-row barley. The sample was planted in four different locations, and the following was also carried out: phenotyping, genotyping and association analysis.

Results: In total, 64 SNPs (on 2H, 4H and 5H chromosomes) significantly associated with productivity traits were revealed in the sample studied, which consisted of two- and six-row barley varieties. No significant loci were identified when conducting association

analysis with row-type covariate. Accordingly, it turns out that all markers identified by GWAS will be correlated with genes that affect row-type. Next, a genome-wide association analysis was carried out only on 68 two-row varieties, which made it possible to revealed 42 SNPs on chromosomes 1H, 2H, 4H and 7H. This was confirmed by an association analysis of a sample consisting of 129 varieties of two-row barley at other locations. In both analyzes, both for only two-row barley and for combined 2/6-row barley, only the locus on chromosome 2H was common.

Conclusion: Our study represents a search for loci related to row type determination. It was found that genes controlling the rowing of the spike make a large contribution in the combined samples. Eleven chromosome regions were identified using GWAS. One of confirmed loci was previously described in the literature. The presence of a new chip of higher density allows more targeted detection of row-associated loci. We performed an experiment lasting for three consecutive years under different natural conditions and studied the effect of rowing on such agronomic traits as “spike length”, “number of grains per main spike”, “weight of 1000 grains”, and “grain weight of the main spike”.

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